



SEQUENCE LISTING

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TECH CENTER 1600/2900

<110> Logemann, Juergen
Jach, Guido
Gornhardt, Birgit
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Schell, Jeff
Eckes, Peter
Chet, Ilan

<120> Transgenic pathogen-resistant organism

<130> A29542-FWC-I-R 070037.0195

<140> US 09/729,141

<141> 2000-12-01

<150> 08/812,025

<151> 1997-03-06

<150> 08/457,797

<151> 1995-06-01

<150> 08/134,416

<151> 1993-10-08

<160> 12

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 275

<212> DNA

<213> Aspergillus giganteus

<220>

<221> CDS

<222> (46)...(225)

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Met Gln Glu Met

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Arg Ala Arg Val Leu Ala Thr Tyr Asn Gly Lys Cys Tyr Lys Lys Asp

5	10	15	20	
aat atc tgc aag tac aag gca cag agc ggc aag act gcc att tgc aag	153			
Asn Ile Cys Lys Tyr Lys Ala Gln Ser Gly Lys Thr Ala Ile Cys Lys				
25 30 35				
tgc tat gtc aaa aag tgc ccc cgc gac ggc gcg aaa tgc gag ttt gac	201			
Cys Tyr Val Lys Lys Cys Pro Arg Asp Gly Ala Lys Cys Glu Phe Asp				
40 45 50				
agc tac aag ggg aag tgc tac tgc tagacggtga gcgaagggac gaagtaggct	255			
Ser Tyr Lys Gly Lys Cys Tyr Cys				
55 60				
ggggggttatt ttactctgct	275			

agg acg gct gta cag gcc gcc aac acg ctg ggg atc ctg ctg ttc gtg 822
 Arg Thr Ala Val Gln Ala Ala Asn Thr Leu Gly Ile Leu Leu Phe Val
 245 250 255 260

gag gtg ccg ggt ggg ttg acg gtg gcc aag gcg ctg gag ctg ttc cat 870
 Glu Val Pro Gly Gly Leu Thr Val Ala Lys Ala Leu Glu Leu Phe His
 265 270 275

gcg agt ggt ggg aaa taggtagttt tccaggtata cctgcatggg tagtgtaaaa 925
 Ala Ser Gly Gly Lys
 280

gtcgaataaa catgtcacag agtgacggac tgatataaat aaataaataa acgtgtcaca 985
 gagttacata taaacaaata aataaataat taaaaatgtc cagttta 1032

<210> 5

<211> 281

<212> PRT

<213> Hordeum vulgare

<400> 5

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 20 25 30
 Gly Ile Arg Asn Lys Leu Arg Asn Pro Ala His Phe Ser His Asn Arg
 35 40 45
 Pro Val Leu Pro Pro Val Glu Pro Asn Val Pro Pro Ser Arg Trp Phe
 50 55 60
 His Val Val Leu Lys Ala Ser Pro Thr Ser Ala Gly Leu Thr Leu Ala
 65 70 75 80
 Ile Arg Ala Asp Asn Ile Tyr Leu Glu Gly Phe Lys Ser Ser Asp Gly
 85 90 95

Thr Trp Trp Glu Leu Thr Pro Gly Leu Ile Pro Gly [Gly] Ala Thr Tyr Val
 100 105 110

Gly Phe Gly Gly Thr Tyr Arg Asp Leu Leu Gly Asp Thr Asp Lys Leu
 115 120 125

Thr Asn Val Ala Leu Gly Arg Gln Gln Leu [Pro] Ala Asp Ala Val Thr Ala
 130 135 140

Leu His Gly Arg Thr Lys Ala Asp Lys Pro Ser Gly Pro Lys Gln Gln
 145 150 155 160
 Gln Ala Arg Glu Ala Val Thr Thr Leu Leu Met Val Asn Glu Ala
 165 170 175
 Thr Arg Phe Gln Thr Val Ser Gly Phe Val Ala Gly Leu Leu His Pro
 180 185 190
 Lys Ala Val Glu Lys Lys Ser Gly Lys Ile Gly Asn Glu Met Lys Ala
 195 200 205
 Gln Val Asn Gly Trp Gln Asp Leu Ser Ala Ala Leu Leu Lys Thr Asp

ccg gtc gag ccc aac gtc ccg ccg agc agg tgg ttc cac gtc gtg ctc	246
Pro Val Glu Pro Asn Val Pro Pro Ser Arg Trp Phe His Val Val Leu	
55 60 65	
aag gcc tcg ccg acc agc gcc ggg ctc acg ctg gcc att cgg gcg gac	294
Lys Ala Ser Pro Thr Ser Ala Gly Leu Thr Leu Ala Ile Arg Ala Asp	
70 75 80	
aac atc tac ctg gag ggc ttc aag agc agc gac ggc acc tgg tgg gag	342
Asn Ile Tyr Leu Glu Gly Phe Lys Ser Ser Asp Gly Thr Trp Trp Glu	
85 90 95 100	
ctc acc ccg ggc ctc atc ccc ggc gcc acc tac gtc ggg ttc ggc ggc	390
Leu Thr Pro Gly Leu Ile Pro Gly Ala Thr Tyr Val Gly Phe Gly Gly	
105 110 115	
acc tac cgc gac ctc ctc ggc gac acc gac aag ctg acc aac gtc gct	438
Thr Tyr Arg Asp Leu Leu Gly Asp Thr Asp Lys Leu Thr Asn Val Ala	
120 125 130	
CTC GGC CGG CAG CAG [CTC CCG] CTG GCG GAC GCG GTG ACC GCC CTC CAC GGG CGC	486
Leu Gly Arg Gln Gln [Leu Ala] Leu Ala Asp Ala Val Thr Ala Leu His Gly Arg	
135 140 145	
acc aag gcc gac aag ccg tcc ggc ccg aag cag cag cag gcg agg gag	534
Thr Lys Ala Asp Lys Pro Ser Gly Pro Lys Gln Gln Gln Ala Arg Glu	
150 155 160	
gcg gtg acg acg ctg ctc ctc atg gtg aac gag gcc acc cgg ttc cag	582
Ala Val Thr Thr Leu Leu Met Val Asn Glu Ala Thr Arg Phe Gln	
165 170 175 180	
acg gtg tct ggg ttc gtg gcc ggg ttg ctg cac ccc aag gcg gtg gag	630
Thr Val Ser Gly Phe Val Ala Gly Leu Leu His Pro Lys Ala Val Glu	
185 190 195	
aag aag agc ggg aag atc ggc aat gag atg aag gcc cag gtg aac ggg	678
Lys Lys Ser Gly Lys Ile Gly Asn Glu Met Lys Ala Gln Val Asn Gly	
200 205 210	
tgg cag gac ctg tcc gcg gcg ctg ctg aag acg gac gtg aag cct ccg	726
Trp Gln Asp Leu Ser Ala Ala Leu Leu Lys Thr Asp Val Lys Pro Pro	
215 220 225	
ccg gga aag tcg cca gcg aag ttc gcg ccg atc gag aag atg ggc gtg	774
Pro Gly Lys Ser Pro Ala Lys Phe Ala Pro Ile Glu Lys Met Gly Val	
230 235 240	

210		215		220
Val Lys Pro Pro Pro Gly Lys Ser Pro Ala Lys Phe Ala Pro Ile Glu				
225		230		235
Lys Met Gly Val Arg Thr Ala Val Gln Ala Ala Asn Thr Leu Gly Ile				
		245		250
Leu Leu Phe Val Glu Val Pro Gly Gly Leu Thr Val Ala Lys Ala Leu				
		260		265
Glu Leu Phe His Ala Ser Gly Gly Lys				270
		275		280

<210> 6
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 <213> Hordeum vulgare

<220>
 <221> CDS
 <222> (1)...(351)
 <223> protein syntheis inhibitor (PSI), aminoterminally
 incomplete protein from an incomplete PSI cDNA
 clone

<221> 3'UTR
 <222> (352)...(487)

<221> polyA_signal
 <222> (404)...(409)
 <223> potential polyadenylation signal

<221> polyA_signal
 <222> (437)...(442)
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<221> polyA_signal
 <222> (445)...(450)
 <223> potential polyadenylation signal

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 acg gtg tcg ggg ttc gtg gcc ggg ctg ctg cac ccc aag gcg gtg gag 96
 Thr Val Ser Gly Phe Val Ala Gly Leu Leu His Pro Lys Ala Val Glu
 20 25 30

 aag aag agc ggg aag atc ggc aat gag atg aag gcc cag gtg aac ggg 144

Lys Lys Ser Gly Lys Ile Gly Asn Glu Met Lys Ala Gln Val Asn Gly
 35 40 45

tgg cag gac ctg tcc gcg gcg ctg ctg aag acg gac gtg aag ccc ccg 192
 Trp Gln Asp Leu Ser Ala Ala Leu Leu Lys Thr Asp Val Lys Pro Pro
 50 55 60

ccg gga aag tcg cca gcg aag ttc acg ccg atc gag aag atg ggc gtg 240
 Pro Gly Lys Ser Pro Ala Lys Phe Thr Pro Ile Glu Lys Met Gly Val
 65 70 75 80

agg act gct gag cag gct gcg gct act ttg ggg atc ctg ctg ttc gtt 288
 Arg Thr Ala Glu Gln Ala Ala Ala Thr Leu Gly Ile Leu Leu Phe Val
 85 90 95

gag gtg ccg ggt ggg ttg acg gtg gcc aag gcg ctg gag ctg ttt cat 336
 Glu Val Pro Gly Gly Leu Thr Val Ala Lys Ala Leu Glu Leu Phe His
 100 105 110

gcg agt ggt ggg aaa taggtagttt tgcaggtata cctgcatggg taaatgtaaa 391
 Ala Ser Gly Gly Lys
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agtcgaataa aaatgtcaca gagtgacgga ctgatataaa taaattaata aacatgtcat 451
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<210> 7

<211> 117

<212> PRT

<213> Hordeum vulgare

<400> 7

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 20 25 30
 Lys Lys Ser Gly Lys Ile Gly Asn Glu Met Lys Ala Gln Val Asn Gly
 35 40 45
 Trp Gln Asp Leu Ser Ala Ala Leu Leu Lys Thr Asp Val Lys Pro Pro
 50 55 60
 Pro Gly Lys Ser Pro Ala Lys Phe Thr Pro Ile Glu Lys Met Gly Val
 65 70 75 80
 Arg Thr Ala Glu Gln Ala Ala Ala Thr Leu Gly Ile Leu Leu Phe Val
 85 90 95
 Glu Val Pro Gly Gly Leu Thr Val Ala Lys Ala Leu Glu Leu Phe His
 100 105 110
 Ala Ser Gly Gly Lys
 115

<210> 8
<211> 2329
<212> DNA
<213> *Serratia marcescens*

<220>
<221> misc_feature
<222> (1)...(2329)
<223> ChiS gene from plasmid pLChis from E.coli A5187

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atztatcttt ccttaataga aaattcacta tccttatttg tcatgttttc ttttatttat 120
atgaaaataa attcacgctt gctgaataaa acccagttga tagcgctctt gtttttgcgc 180
cttttttatt tatagtactg aatgtacgcg gtgggaatga ttatttcgcc acgtggaaag 240
acgctgttgt tatttattga ttttaacctt cgcggattat tgcggaattt tttcgcttcg 300
gcaatgcata gcgacgatta actcttttat gtttatcctc tcggaataaa ggaatcagtt 360
atgcgcaa at ttaataaacc gctgttggcg ctgttgatcg gcagcacgct gtgttcgcgc 420
gcgcaggccg ccgcgccggg caagccgacc atcgccctggg gcaacaccaa gttcgccatc 480
gttgaagttg accaggcggc taccgcttat aataatttgg tgaaggtaaa aaatgccgcc 540
gatgtttccg tctcctggaa tttatggaat ggcgacaccg gcacgacggc aaaagtttta 600
ttaaatggca aagaggcggt gagtggtcct tcaaccggat cttccggtag ggcgaatttt 660
aaagtgaata aaggcggccg ttatcaa atg caggtggcac tgtgcaatgc cgacggctgc 720
accgccagt acgccaccga aattgtggtg gccgacaccg acggcagcca tttggcgccg 780
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gcgcaaaacc tgaccacact gctgtacggc tttatcccga tctgcggcgg caatggcatc 960
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ggcgtgaccg cctgggatga cccctacaag ggcaacttcg gccagctgat ggcgctgaag 1140
caggcgcatc ctgacctgaa aatcctgccg tcgatcggcg gctggacgct gtccgaccgc 1200
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gagctgcggg cgatgctgga tcagctgtcg gtggaaaccg gccgcaagta tgagctgacc 1440
tccgccatca gcgccggtaa ggacaagatc gacaagggtg cttacaacgt tgcgcagaac 1500
tcgatggatc acatcttcct gatgagctac gacttctatg gcgccttcga tctgaagaac 1560
ctggggcatc agaccgcgct gaatgcgccg gcctggaaac cggacaccgc ctacaccacg 1620
gtgaacggcg tcaatgcgct gctggcgagc ggcgtaagc cgggcaaaat cgtcgtcggc 1680
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accggcaccg ccaccggggc ggttaaaggc acctgggaga acggtatcgt ggactaccgc 1800
caaatcgccg gccagttcat gagcggcgag tggcagtata cctacgacgc cacggcgga 1860
gcgccttacg tgttcaaacc ttccaccggc gatctgatca cttcgcacga tgcccgtcgc 1920
gtgcaggcta aaggcaagta cgtgttgat aagcagctgg gcggcctgtt ctccctgggag 1980
atcgacgcgg ataacggcga tattctcaac agcatgaacg ccagcctggg caacagcgcc 2040
ggcgttcaat aatcggttgc agtggttgcc gggggatatc ctttcgcccc cggctttttc 2100


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gccgacgaaa gttttttttac gccgcacaga ttgtggctct gccccgagca aaacgcgctc 2160
atcggactca cccttttggg taatccttca gcatttcctc ctgtctttaa cggcgatcac 2220
aaaaataacc gttcagatat tcatcattca gcaacaaagt ttggcggtt tttaacggag 2280
ttaaaaacca gtaagtttgt gagggtcaga ccaatgcgct aaaaatggg 2329

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<210> 9

<211> 1002

<212> DNA

<213> Hordeum vulgare

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<221> 5'UTR

<222> (1)...(63)

<221> CDS

<222> (64)...(861)

<223> 26 kD preprotein of chitinase (ChiG)

<221> 3'UTR

<222> (862)...(1002)

<223> partial, 11 nucleotides at 3' end not shown

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<222> (905)...(910)

<223> potential polyadenylation site

<221> sig_peptide

<222> (64)...(294)

<223> probable signal peptide

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<222> (298)...(312)

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<221> sig_peptide

<222> (349)...(378)

<223> probable signal peptide

<221> sig_peptide

<222> (466)...(588)

<223> probable signal peptide

<221> sig_peptide

<222> (607)...(861)

<223> probable signal peptide

<221> mat_peptide

<222> (133)...(861)

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Met Arg Ser Leu Ala Val Val Val Ala Val Val Ala Thr Val Ala	
1 5 10 15	
atg gcc atc ggc acg gcg cgc ggc agc gtg tcc tcc atc gtc tcg cgc	156
Met Ala Ile Gly Thr Ala Arg Gly Ser Val Ser Ser Ile Val Ser Arg	
20 25 30	
gca cag ttt gac cgc atg ctt ctc cac cgc aac gac ggc gcc tgc cag	204
Ala Gln Phe Asp Arg Met Leu Leu His Arg Asn Asp Gly Ala Cys Gln	
35 40 45	
gcc aag ggc ttc tac acc tac gac gcc ttc gtc gcc gcc gca gcc gcc	252
Ala Lys Gly Phe Tyr Thr Tyr Asp Ala Phe Val Ala Ala Ala Ala Ala	
50 55 60	
ttc ccg ggc ttc ggc acc acc ggc agc gcc gac gcc cag aag cgc gag	300
Phe Pro Gly Phe Gly Thr Thr Gly Ser Ala Asp Ala Gln Lys Arg Glu	
65 70 75	
gtg gcc gcc ttc cta gca cag acc tcc cac gag acc acc ggc ggg tgg	348
Val Ala Ala Phe Leu Ala Gln Thr Ser His Glu Thr Thr Gly Gly Trp	
80 85 90 95	
gcg act gca ccg gac ggg gcc ttc gcc tgg ggc tac tgc ttc aag cag	396
Ala Thr Ala Pro Asp Gly Ala Phe Ala Trp Gly Tyr Cys Phe Lys Gln	
100 105 110	
gaa cgt ggc gcc tcc tcc gac tac tgc acc ccg agc gca caa tgg ccg	444
Glu Arg Gly Ala Ser Ser Asp Tyr Cys Thr Pro Ser Ala Gln Trp Pro	
115 120 125	
tgc gcc ccc ggg aag cgc tac tac ggc cgc ggg cca atc cag ctc tcc	492
Cys Ala Pro Gly Lys Arg Tyr Tyr Gly Arg Gly Pro Ile Gln Leu Ser	
130 135 140	
cac aac tac aac tat gga cct gcc ggc cgg gcc atc ggg gtc gat ctg	540
His Asn Tyr Asn Tyr Gly Pro Ala Gly Arg Ala Ile Gly Val Asp Leu	
145 150 155	
ctg gcc aac ccg gac ctg gtg gcc acg gac gcc act gtg ggc ttt aag	588
Leu Ala Asn Pro Asp Leu Val Ala Thr Asp Ala Thr Val Gly Phe Lys	
160 165 170 175	

acg gcc atc tgg ttc tgg atg acg gcg cag ccg ccc aag cca tcg agc 636
 Thr Ala Ile Trp Phe Trp Met Thr Ala Gln Pro Pro Lys Pro Ser Ser
 180 185 190

cat gct gtg atc gcc ggc cag tgg agc ccg tca ggg gct gac cgg gcc 684
 His Ala Val Ile Ala Gly Gln Trp Ser Pro Ser Gly Ala Asp Arg Ala
 195 200 205

gca ggc cgg gtg ccc ggg ttt ggt gtg atc acc aac atc atc aac ggc 732
 Ala Gly Arg Val Pro Gly Phe Gly Val Ile Thr Asn Ile Ile Asn Gly
 210 215 220

ggg atc gag tgc ggt cac ggg cag gac agc cgc gtc gcc gat cga atc 780
 Gly Ile Glu Cys Gly His Gly Gln Asp Ser Arg Val Ala Asp Arg Ile
 225 230 235

ggg ttt tac aag cgc tac tgt gac atc ctc ggc gtt ggc tac ggc aac 828
 Gly Phe Tyr Lys Arg Tyr Cys Asp Ile Leu Gly Val Gly Tyr Gly Asn
 240 245 250 255

aac ctc gat tgc tac agc cag aga ccc ttc gcc taattaatta gtcattgtatt 881
 Asn Leu Asp Cys Tyr Ser Gln Arg Pro Phe Ala
 260 265

aatcttggcc ctccataaaa tacaataaga gcatcgtctc ctatctacat gctgtaagat 941
 gtaactatgg taacctttta tggggaacat aacaaaggca tctcgtatag atgctttgct 1001
 a 1002

<210> 10

<211> 266

<212> PRT

<213> Hordeum vulgare

<400> 10

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 Gln Phe Asp Arg Met Leu Leu His Arg Asn Asp Gly Ala Cys Gln Ala
 35 40 45
 Lys Gly Phe Tyr Thr Tyr Asp Ala Phe Val Ala Ala Ala Ala Phe
 50 55 60
 Pro Gly Phe Gly Thr Thr Gly Ser Ala Asp Ala Gln Lys Arg Glu Val
 65 70 75 80
 Ala Ala Phe Leu Ala Gln Thr Ser His Glu Thr Thr Gly Gly Trp Ala
 85 90 95

Thr	Ala	Pro	Asp	Gly	Ala	Phe	Ala	Trp	Gly	Tyr	Cys	Phe	Lys	Gln	Glu
			100					105					110		
Arg	Gly	Ala	Ser	Ser	Asp	Tyr	Cys	Thr	Pro	Ser	Ala	Gln	Trp	Pro	Cys
		115					120					125			
Ala	Pro	Gly	Lys	Arg	Tyr	Tyr	Gly	Arg	Gly	Pro	Ile	Gln	Leu	Ser	His
		130				135					140				
Asn	Tyr	Asn	Tyr	Gly	Pro	Ala	Gly	Arg	Ala	Ile	Gly	Val	Asp	Leu	Leu
145					150					155					160
Ala	Asn	Pro	Asp	Leu	Val	Ala	Thr	Asp	Ala	Thr	Val	Gly	Phe	Lys	Thr
				165					170					175	
Ala	Ile	Trp	Phe	Trp	Met	Thr	Ala	Gln	Pro	Pro	Lys	Pro	Ser	Ser	His
			180					185					190		
Ala	Val	Ile	Ala	Gly	Gln	Trp	Ser	Pro	Ser	Gly	Ala	Asp	Arg	Ala	Ala
		195					200					205			
Gly	Arg	Val	Pro	Gly	Phe	Gly	Val	Ile	Thr	Asn	Ile	Ile	Asn	Gly	Gly
		210				215					220				
Ile	Glu	Cys	Gly	His	Gly	Gln	Asp	Ser	Arg	Val	Ala	Asp	Arg	Ile	Gly
225					230					235					240
Phe	Tyr	Lys	Arg	Tyr	Cys	Asp	Ile	Leu	Gly	Val	Gly	Tyr	Gly	Asn	Asn
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Leu	Asp	Cys	Tyr	Ser	Gln	Arg	Pro	Phe	Ala						
			260					265							

<210> 11
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 <212> DNA
 <213> Hordeum vulgare

<220>
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 <222> (1)...(48)

 <221> CDS
 <222> (49)...(1050)
 <223> preprotein of the glucanase GluG

<221> 3'UTR
 <222> (1051)...(1235)
 <223> partial, 14 nucleotides at the 3' end not shown

<221> polyA_signal
 <222> (1083)...(1088)
 <223> potential polyadenylation signal

<221> polyA_signal
 <222> (1210)...(1215)
 <223> potential polyadenylation signal

<221> mat_peptide
<222> (133)...(1050)

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                                     Met Ala Arg
                                     1

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Lys Asp Val Ala Ser Met Phe Ala Val Ala Leu Phe Ile Gly Ala Phe
      5                      10                      15

gct gct gtt cct acg agt gtg cag tcc atc ggc gta tgc tac ggc gtg 153
Ala Ala Val Pro Thr Ser Val Gln Ser Ile Gly Val Cys Tyr Gly Val
      20                      25                      30                      35

atc ggc aac aac ctc ccc tcc cgg agc gac gtg gtg cag ctc tac agg 201
Ile Gly Asn Asn Leu Pro Ser Arg Ser Asp Val Val Gln Leu Tyr Arg
                        40                      45                      50

tcc aag ggc atc aac ggc atg cgc atc tac ttc gcc gac ggg cag gcc 249
Ser Lys Gly Ile Asn Gly Met Arg Ile Tyr Phe Ala Asp Gly Gln Ala
                        55                      60                      65

ctc tcg gcc gtc cgc aac tcc ggc atc ggc ctc atc ctc gac atc ggc 297
Leu Ser Ala Val Arg Asn Ser Gly Ile Gly Leu Ile Leu Asp Ile Gly
      70                      75                      80

aac gac cag ctc gcc aac atc gcc gcc agc acc tcc aac gcg gcc tcc 345
Asn Asp Gln Leu Ala Asn Ile Ala Ala Ser Thr Ser Asn Ala Ala Ser
      85                      90                      95

tgg gtc cag aac aac gtg cgg ccc tac tac cct gcc gtg aac atc aag 393
Trp Val Gln Asn Asn Val Arg Pro Tyr Tyr Pro Ala Val Asn Ile Lys
100                      105                      110                      115

tac atc gcc gcc ggc aac gag gtg cag ggc ggc gcc acg cag agc atc 441
Tyr Ile Ala Ala Gly Asn Glu Val Gln Gly Gly Ala Thr Gln Ser Ile
                        120                      125                      130

ctg ccg gcc atg cgc aac ctc aac gcg gcc ctc tcc gcg gcg ggg ctc 489
Leu Pro Ala Met Arg Asn Leu Asn Ala Ala Leu Ser Ala Ala Gly Leu
                        135                      140                      145

ggc gcc atc aag gtg tcc acc tcc atc cgg ttc gac gag gtg gcc aac 537
Gly Ala Ile Lys Val Ser Thr Ser Ile Arg Phe Asp Glu Val Ala Asn
      150                      155                      160
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tcc ttc ccg ccc tcc gcc ggc gtg ttc aag aac gcc tac atg acg gac	585
Ser Phe Pro Pro Ser Ala Gly Val Phe Lys Asn Ala Tyr Met Thr Asp	
165 170 175	
gtg gcc cgg ctc ctg gcg agc acc ggc gcg ccg ctg ctc gcc aac gtc	633
Val Ala Arg Leu Leu Ala Ser Thr Gly Ala Pro Leu Leu Ala Asn Val	
180 185 190 195	
tac ccc tac ttc gcg tac cgt gac aac ccc ggg agc atc agc ctg aac	681
Tyr Pro Tyr Phe Ala Tyr Arg Asp Asn Pro Gly Ser Ile Ser Leu Asn	
200 205 210	
tac gcg acg ttc cag ccg ggc acc acc gtg cgt gac cag aac aac ggg	729
Tyr Ala Thr Phe Gln Pro Gly Thr Thr Val Arg Asp Gln Asn Asn Gly	
215 220 225	
ctg acc tac acg tcc ctg ttc gac gcg atg gtg gac gcc gtg tac gcg	777
Leu Thr Tyr Thr Ser Leu Phe Asp Ala Met Val Asp Ala Val Tyr Ala	
230 235 240	
gcg ctg gag aag gcc ggc gcg ccg gcg gtg aag gtg gtg gtg tcg gag	825
Ala Leu Glu Lys Ala Gly Ala Pro Ala Val Lys Val Val Val Ser Glu	
245 250 255	
agc ggg tgg ccg tcg gcg ggc ggg ttt gcg gcg tcg gcc ggc aat gcg	873
Ser Gly Trp Pro Ser Ala Gly Gly Phe Ala Ala Ser Ala Gly Asn Ala	
260 265 270 275	
cgg acg tac aac cag ggg ctg atc aac cac gtc ggc ggg ggc acg ccc	921
Arg Thr Tyr Asn Gln Gly Leu Ile Asn His Val Gly Gly Gly Thr Pro	
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Lys Lys Arg Glu Ala Leu Glu Thr Tyr Ile Phe Ala Met Phe Asn Glu	
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Asn Gln Lys Thr Gly Asp Ala Thr Glu Arg Ser Phe Gly Leu Phe Asn	
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Pro Asp Lys Ser Pro Ala Tyr Asn Ile Gln Phe	
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 35 40 45
 Leu Tyr Arg Ser Lys Gly Ile Asn Gly Met Arg Ile Tyr Phe Ala Asp
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 Gly Gln Ala Leu Ser Ala Val Arg Asn Ser Gly Ile Gly Leu Ile Leu
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 Asp Ile Gly Asn Asp Gln Leu Ala Asn Ile Ala Ala Ser Thr Ser Asn
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 Ala Ala Ser Trp Val Gln Asn Asn Val Arg Pro Tyr Tyr Pro Ala Val
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 Asn Ile Lys Tyr Ile Ala Ala Gly Asn Glu Val Gln Gly Gly Ala Thr
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 Gln Ser Ile Leu Pro Ala Met Arg Asn Leu Asn Ala Ala Leu Ser Ala
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 Ala Gly Leu Gly Ala Ile Lys Val Ser Thr Ser Ile Arg Phe Asp Glu
 145 150 155 160
 Val Ala Asn Ser Phe Pro Pro Ser Ala Gly Val Phe Lys Asn Ala Tyr
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 Met Thr Asp Val Ala Arg Leu Leu Ala Ser Thr Gly Ala Pro Leu Leu
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 Ala Asn Val Tyr Pro Tyr Phe Ala Tyr Arg Asp Asn Pro Gly Ser Ile
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 Ser Leu Asn Tyr Ala Thr Phe Gln Pro Gly Thr Thr Val Arg Asp Gln
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 Asn Asn Gly Leu Thr Tyr Thr Ser Leu Phe Asp Ala Met Val Asp Ala
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 Val Tyr Ala Ala Leu Glu Lys Ala Gly Ala Pro Ala Val Lys Val Val
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 Val Ser Glu Ser Gly Trp Pro Ser Ala Gly Gly Phe Ala Ala Ser Ala
 260 265 270
 Gly Asn Ala Arg Thr Tyr Asn Gln Gly Leu Ile Asn His Val Gly Gly
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 Gly Thr Pro Lys Lys Arg Glu Ala Leu Glu Thr Tyr Ile Phe Ala Met
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 Phe Asn Glu Asn Gln Lys Thr Gly Asp Ala Thr Glu Arg Ser Phe Gly
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 Leu Phe Asn Pro Asp Lys Ser Pro Ala Tyr Asn Ile Gln Phe

325

330